

SEQUENCE LISTING

<110> Rajgarhia, Vineet

<120> Methods and materials for synthesis of organic products

<130> 00-1237-A

<140> 09

<141> 2001-11-23

<150> 60/252,541

<151> 2000-11-22

<160> 65

<170> PatentIn version 3.1

<210> 1

<211> 92

<212> DNA

<213> artificial sequence - multiple cloning site

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gccgcctcga gtctagaggg cccaagcttg gg
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<213> artificial sequence - multiple cloning site

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gcagggatcc cccgggggaat tcaagcttgg g
91

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<211> 31

<212> DNA

<213> Lactobacillus helveticus

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<210> 4

<211> 32

<212> DNA

<213> Lactobacillus helveticus

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ccaagatctt tattgacgaa ccttaacgcc ag
32

<210> 5

<211> 37

<212> DNA

<213> Pediococcus acidilactici

<400> 5

ccgggatcca tgtctaatat tcaaaatcat caaaaag
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<210> 6

<211> 33

<212> DNA

<213> Pediococcus acidilactici

<400> 6

ccaagatctt tatttgtctt gtttttcagc aag
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<210> 7

<211> 82

<212> DNA

<213> Kluyveromyces marxianus

<400> 7

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ctttttctttt tttttctttt ct

82

<210> 8

<211> 79

<212> DNA

<213> Kluyveromyces marxianus

<400> 8

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gccggtagag gtgtggtca

79

<210> 9

<211> 1736

<212> DNA

<213> kanamycin resistance gene

<400> 9

gtacaacttg agcaagttgt cgatcagctc ctcaaattgg tcctctgtaa cggatgactc

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aacttgcaca ttaacttgaa gctcagtcga ttgagtgaac ttgatcaggt tgtgcagctg

120

gtcagcagca tagggaaaca cggcttttcc taccaaactc aaggaattat caaactctgc

180

aacacttgcg tatgcaggta gcaagggaaa tgtcatactt gaagtcggac agtgagtgta

240

gtcttgagaa attctgaagc cgtattttta ttatcagtga gtcagtcac aggagatcct

300

ctacgccgga cgcacgtgg ccgacctgca gggggggggg gggcgctgag gtctgcctcg

360

tgaagaaggt gttgctgact cataccaggc ctgaatcgcc ccatcatcca gccagaaagt

420

gagggagcca cggttgatga gagctttggt gtaggtggac cagttggtga ttttgaactt

480

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540

agcaaaagtt cgattttattc aacaaagccg ccgtcccgtc aagtcagcgt aatgctctgc
600

cagtgttaca accaattaac caattctgat tagaaaaact catcgagcat caaatgaaac
660

tgcaatttat tcatatcagg attatcaata ccatatTTTT gaaaaagccg tttctgtaat
720

gaaggagaaa actcaccgag gcagttccat aggatggcaa gatcctggta tcggtctgcg
780

attccgactc gtccaacatc aatacaacct ttaatttccc ctggtcaaaa ataaggttat
840

caagtgagaa atcaccatga gtgacgactg aatccggtga gaatggcaaa agcttatgca
900

ttctttccag acttggtcaa caggccagcc attacgctcg tcatcaaaat cactcgcac
960

aaccaaaccg ttattcattc gtgattgcgc ctgagcgcga cgaaatacgc gatcgctggt
1020

aaaaggacaa ttacaaacag gaatcgaatg caaccggcgc aggaacactg ccagcgcac
1080

aacaatatTT tccactgaat caggatatTC ttctaatacc tggaatgctg ttttcccggg
1140

gatcgcagtg gtgagtaacc atgcatcac aggagtacgg ataaaatgct tgatgggtcgg
1200

aagaggcata aattccgtca gccagtttag tctgaccatc tcatctgtaa catcattggc
1260

aacgctacct ttgccatggt tcagaaacaa ctctggcgca tcgggcttcc catacaatcg
1320

atagattgtc gcacctgatt gcccgacatt atcgcgagcc catttatacc catataaatc
1380

agcatccatg ttggaattta atcgcggcct cgagcaagac gtttcccgtt gaatatggct
1440

cataacaccc cttgtattac tgtttatgta agcagacagt tttattgttc atgatgatat
1500

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1560

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1620

catcacccgat ggggaagatc gggctcgcca ctteggggctc atgagcgctt gtttcggcgt
1680

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1736

<210> 10

<211> 372

<212> DNA

<213> Kluyveromyces marxianus

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tgaccaaggt caaggatgct gctaagggtt acaagccagt tccagttcct cacgctccaa
180

gagacaacaa gccagttgct gactctactc cattgaagca agaatgggtc tggactcaag
240

tcggtaagtt cctacaagaa ggtgatgttg ttctaactga aaccgggtacc tccgctttcg
300

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ccattgggtt ca
372

<210> 11
<211> 747
<212> DNA
<213> Kluyveromyces thermotolerans

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120

acgcttacgc cagaatcaag ggtatgtcct gtttgatcac caccttcggt gtcggtgagt
180

tgtecgcttt gaacgggtatc gccgggttctt acgctgagca cgtcgggtgtc ttgcacattg
240

tcgggtgtccc atccgtctcc gcccaggcca agcagctatt gttgcaccac accttgggta
300

acgggtgactt cactgtcttc cacagaatgt ccgccaacat ctctgagacc actgctatga
360

tcactgatct agctaccgcc ccactctgaga tcgacagatg tatcagaacc acctacatta
420

gacagagacc tgtctacttg ggtttgccat ctaacttcgt tgaccagatg gtcccagcct
480

ctctattgga caccccaatt gacttggcct tgaagccaaa cgaccagcag gctgaggagg
540

aggtcacctc tactttgttg gagatgatca aggacgctaa gaaccagtc atcttggctg
600

acgcttgccg ttccagacac gatgtcaagg ctgagaccaa gaagttgatt gacatcactc
660

agttcccatc tttegttacc ccaatgggta agggttccat tgacgagaag caccacaagat
720

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747

<210> 12
<211> 1738
<212> DNA
<213> kanalycin resistance gene fragment

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120

gtcagcagca tagggaaaca cggcttttcc taccaaactc aaggaattat caaactctgc
180

aacacttgcg tatgcaggta gcaagggaaa tgtcatactt gaagtcggac agtgagtgta
240

gtcttgagaa attctgaagc cgtattttta ttatcagtga gtcagtcac aggagatcct
300

ctacgccgga cgcacgtgg cgcacctgca gggggggggg gggcgctgag gtctgcctcg
360

tgaagaaggt gttgctgact cataccaggc ctgaatcgcc ccatcatcca gccagaaagt
420

gagggagcca cggttgatga gagctttggt gtaggtggac cagttggtga ttttgaactt
480

ttgctttgcc acggaacggt ctgcggtgtc gggaagatgc gtgatctgat ccttcaactc
540

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600

cagtgttaca accaattaac caattctgat tagaaaaact catcgagcat caaatgaaac
660

tgcaatttat tcatatcagg attatcaata ccatattttt gaaaaagccg tttctgtaat
720

gaaggagaaa actcaccgag gcagttccat aggatggcaa gatcctggta tcggtctgcg
780

attccgactc gtccaacatc aatacaacct attaatctcc cctcgtcaaa aataaggtta
840

tcaagtgaga aatcaccatg agtgacgact gaatccggtg agaatggcaa aagcttatgc
900

atttctttcc agacttggtc aacaggccag ccattacgct cgtcatcaaa atcactcgca
960

tcaaccaaac cgttattcat tcgtgattgc gcctgagcga gacgaaatac gcgatcgctg
1020

ttaaaaggac aattacaaac aggaatcgaa tgcaaccggc gcaggaacac tgccagcgca
1080

tcaacaatat tttcacctga atcaggatat tcttctaata cctggaatgc tgttttcccg
1140

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1200

ggaagaggca taaattccgt cagccagttt agtctgacca tctcatctgt aacatcattg
1260

gcaacgctac ctttgccatg tttcagaaac aactctggcg catcgggctt cccatacaat
1320

cgatagattg tcgcacctga ttgcccgcga ttatcgcgag cccatttata cccatataaa
1380

tcagcatcca tgttggaatt taatcgcggc ctcgagcaag acgtttcccg ttgaatatgg
1440

ctcataacac cccttggtatt actgtttatg taagcagaca gttttattgt tcatgatgat
1500

atatttttat cttgtgcaat gtaacatcag agattttgag acacaacgtg gctttccccc
1560

ccccccctgc aggtcggcat caccggcgcc acaggtgcgg ttgctggcgc ctatatcgcc
1620

gacatcaccg atggggaaga tcgggctcgc cacttcgggc tcatgagcgc ttgtttcggc
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1738

<210> 13
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<212> DNA
<213> artificial sequence - degenerate amplification primers

<400> 13
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<210> 14
<211> 17
<212> DNA
<213> artificial sequence - degenerate amplification primers

<400> 14
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<210> 15
<211> 22
<212> DNA
<213> artificial sequence - amplification primers

<400> 15
gtacagttct ggatactgct cg
22

<210> 16
<211> 18
<212> DNA
<213> artificial sequence - amplification primers

<400> 16
acaggcatcg atgctgtc
18

<210> 17
<211> 19

<212> DNA

<213> Kluyveromyces thermotolerans

<400> 17

gtgatgtcgg cgatatagg

19

<210> 18

<211> 21

<212> DNA

<213> Kluyveromyces thermotolerans

<400> 18

ctacttggag ccactatcga c

21

<210> 19

<211> 21

<212> DNA

<213> Kluyveromyces thermotolerans

<400> 19

gatctcctgc taagctcttg c

21

<210> 20

<211> 20

<212> DNA

<213> Kluyveromyces thermotolerans

<400> 20

gcagttttgg atattcatgc

20

<210> 21

<211> 972

<212> DNA

<213> Kluyveromyces thermotolerans

<400> 21

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120

gtttccgaga ttgtccttat cgacgtgaac aaagacaaag cagaggggtga aagcatggac
180

ttaaaccacg cagcaccttc aaatacaagg tctcgagcgg gtgattatcc tgactgcgct
240

ggcgcggcca ttgttattgt cacatgtggg attaaccaaa aaaatggaca aacaaggatg
300

gatcttgctg caaaaaatgc caacattatg ctggaaatca tccccaatgt tgccaaatat
360

gctcctgata ccattcctgct tattgccacg aatcctgtcg atgttttgac ctatattagc
420

tataaggcgt cagggtttcc actaagcaga gttatcggct caggtacagt tctggatact
480

gctcgtttta aatacatcct cggagagcac ttcaagatct catcggacag catcgatgcc
540

tgtgtaattg gagaacatgg tgattcgggt gtgcctgtct ggtctcttac caacatcgac
600

ggcatgaagc tccgggatta ctgcgaaaaa gcccaaccaca tatttgatca gaatgcgttc
660

catagaatct ttgagcaaac gcgagacgct gcttacgata tcatcaagcg caaaggctat
720

acttcatatg gaatcgcagc gggattactt cgcatagtaa aggcgatttt agaggataca
780

ggatccacac ttacagtttc aaccgttggg gattattttg gggttgaaca aattgctata
840

agcgtcccta ccaaactcaa taaaagtggg gctcatcaag tggctgaact ttcactcgat
900

gagaaggaaa tagaattgat ggaaaaatca gctagtcaga tcaaatacgt gattgagcat
960

ctggagatca at
972

<210> 22
<211> 323
<212> PRT
<213> Kluyveromyces thermotolerans

<400> 22

Met Phe Gln Asp Thr Lys Ser Gln Ala Val Arg Thr Asp Ala Lys Thr
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Val Lys Val Val Val Val Gly Val Gly Ser Val Gly Ser Ala Thr Ala
20 25 30

Tyr Thr Leu Leu Leu Ser Gly Ile Val Ser Glu Ile Val Leu Ile Asp
35 40 45

Val Asn Lys Asp Lys Ala Glu Gly Glu Ser Met Asp Leu Asn His Ala
50 55 60

Ala Pro Ser Asn Thr Arg Ser Arg Ala Gly Asp Tyr Pro Asp Cys Ala
65 70 75 80

Gly Ala Ala Ile Val Ile Val Thr Cys Gly Ile Asn Gln Lys Asn Gly
85 90 95

Gln Thr Arg Met Asp Leu Ala Ala Lys Asn Ala Asn Ile Met Leu Glu
100 105 110

Ile Ile Pro Asn Val Ala Lys Tyr Ala Pro Asp Thr Ile Leu Leu Ile
115 120 125

Ala Thr Asn Pro Val Asp Val Leu Thr Tyr Ile Ser Tyr Lys Ala Ser
130 135 140

Gly Phe Pro Leu Ser Arg Val Ile Gly Ser Gly Thr Val Leu Asp Thr
 145 150 155 160

Ala Arg Phe Lys Tyr Ile Leu Gly Glu His Phe Lys Ile Ser Ser Asp
 165 170 175

Ser Ile Asp Ala Cys Val Ile Gly Glu His Gly Asp Gly Val Pro Val
 180 185 190

Trp Ser Leu Thr Asn Ile Asp Gly Met Lys Leu Arg Asp Tyr Cys Glu
 195 200 205

Lys Ala Asn His Ile Phe Asp Gln Asn Ala Phe His Arg Ile Phe Glu
 210 215 220

Gln Thr Arg Asp Ala Ala Tyr Asp Ile Ile Lys Arg Lys Gly Tyr Thr
 225 230 235 240

Ser Tyr Gly Ile Ala Ala Gly Leu Leu Arg Ile Val Lys Ala Ile Leu
 245 250 255

Glu Asp Thr Gly Ser Thr Leu Thr Val Ser Thr Val Gly Asp Tyr Phe
 260 265 270

Gly Val Glu Gln Ile Ala Ile Ser Val Pro Thr Lys Leu Asn Lys Ser
 275 280 285

Gly Ala His Gln Val Ala Glu Leu Ser Leu Asp Glu Lys Glu Ile Glu
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Leu Met Glu Lys Ser Ala Ser Gln Ile Lys Ser Val Ile Glu His Leu
 305 310 315 320

Glu Ile Asn

<210> 23
<211> 20
<212> DNA
<213> artificial sequence - degenerate amplification primers

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<210> 24
<211> 17
<212> DNA
<213> artificial sequence - degenerate amplification primers

<400> 24
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<210> 25
<211> 27
<212> DNA
<213> artificial sequence - amplification primers

<400> 25
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<210> 26
<211> 28
<212> DNA
<213> artificial sequence - amplification primers

<400> 26
gtttggttgc tggaagtggg gttgatag
28

<210> 27
<211> 27
<212> DNA

<213> artificial sequence - amplification primers

<400> 27

aacattgaat agcttgctca ggttgtg
27

<210> 28

<211> 28

<212> DNA

<213> artificial sequence - amplification primers

<400> 28

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28

<210> 29

<211> 939

<212> DNA

<213> *Torulaspora pretoriensis*

<220>

<221> CDS

<222> (1) .. (939)

<223>

<400> 29

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48

Met His Arg Cys Ala Lys Val Ala Ile Val Gly Ala Gly Gln Val Gly

1

5

10

15

tcc aca aca gct tac acg tta tta ttg agt agt ttg gtt gct gaa gtg
96

Ser Thr Thr Ala Tyr Thr Leu Leu Leu Ser Ser Leu Val Ala Glu Val

20

25

30

gtg ttg ata gat gtc gat aaa aga aag gtc gaa ggc caa ttt atg gat
144

Val Leu Ile Asp Val Asp Lys Arg Lys Val Glu Gly Gln Phe Met Asp

35

40

45

ctg aac cac gcg gct cct tta acg aag gag tca cga ttc agt gct ggg
192

Leu Asn His Ala Ala Pro Leu Thr Lys Glu Ser Arg Phe Ser Ala Gly

50

55

60

gac tat gaa agt tgt gct gat gct gcg gtt gta atc gta acg ggc ggg
240

Asp Tyr Glu Ser Cys Ala Asp Ala Ala Val Val Ile Val Thr Gly Gly

65

70

75

80

gct aat cag aaa cct ggt caa act aga atg gag cta gcc gag agg aac
288

Ala Asn Gln Lys Pro Gly Gln Thr Arg Met Glu Leu Ala Glu Arg Asn

85

90

95

gtt aaa atc atg cag gaa gtg atc cct aag att gtg aaa tac gcc ccc
336

Val Lys Ile Met Gln Glu Val Ile Pro Lys Ile Val Lys Tyr Ala Pro

100

105

110

aac gca att ttg ctg att gca aca aac cct gtc gat gta ctt acc tat
384

Asn Ala Ile Leu Leu Ile Ala Thr Asn Pro Val Asp Val Leu Thr Tyr

115

120

125

gct agt ttg aaa gcg tcg gga ttc cca gca agc cgg gtt att ggt tct
432

Ala Ser Leu Lys Ala Ser Gly Phe Pro Ala Ser Arg Val Ile Gly Ser

130

135

140

ggg aca gtt ctc gac tct gct cgt ata cag cac aac ctg agc aag cta
480

Gly Thr Val Leu Asp Ser Ala Arg Ile Gln His Asn Leu Ser Lys Leu

145 150 155 160

ttc aat gtt tca tct gaa agt gtc aac gcg ttt att atc ggg gaa cat
528

Phe Asn Val Ser Ser Glu Ser Val Asn Ala Phe Ile Ile Gly Glu His

165 170 175

ggt gac tca agt gtg ccc gtc tgg tcg ctt gct gag att gcc ggc atg
576

Gly Asp Ser Ser Val Pro Val Trp Ser Leu Ala Glu Ile Ala Gly Met

180 185 190

aaa gtg gag gat tac tgt agg cag tcc aag aga aag ttt gac ccc agc
624

Lys Val Glu Asp Tyr Cys Arg Gln Ser Lys Arg Lys Phe Asp Pro Ser

195 200 205

att ctg acc aaa ata tat gag gag tcg cgt gac gcg gca gcc tac atc
672

Ile Leu Thr Lys Ile Tyr Glu Glu Ser Arg Asp Ala Ala Ala Tyr Ile

210 215 220

ata gaa cgc aaa ggc tat acc aat ttc ggg att gca gca ggt ttg gct
720

Ile Glu Arg Lys Gly Tyr Thr Asn Phe Gly Ile Ala Ala Gly Leu Ala

225 230 235 240

agg ata gtg aga gct att ctg aga gat gaa ggt gcc cta tta act gtg
768

Arg Ile Val Arg Ala Ile Leu Arg Asp Glu Gly Ala Leu Leu Thr Val

245

250

255

tct act gta ggt gag cac ttt ggc atg aaa gat gtt tca ttg agt gtt
816

Ser Thr Val Gly Glu His Phe Gly Met Lys Asp Val Ser Leu Ser Val

260

265

270

cca act agg gta gac agg agc ggc gct cac cat gtc gtc gac ctt ctg
864

Pro Thr Arg Val Asp Arg Ser Gly Ala His His Val Val Asp Leu Leu

275

280

285

cta aac gac aag gag ctg gag caa att aaa aca tct gga gcc aag ata
912

Leu Asn Asp Lys Glu Leu Glu Gln Ile Lys Thr Ser Gly Ala Lys Ile

290

295

300

aag tca gcc tgt gat gaa ctt ggc att
939

Lys Ser Ala Cys Asp Glu Leu Gly Ile

305

310

<210> 30

<211> 313

<212> PRT

<213> *Torulaspora pretoriensis*

<400> 30

Met His Arg Cys Ala Lys Val Ala Ile Val Gly Ala Gly Gln Val Gly
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20 25 30

Val Leu Ile Asp Val Asp Lys Arg Lys Val Glu Gly Gln Phe Met Asp
35 40 45

Leu Asn His Ala Ala Pro Leu Thr Lys Glu Ser Arg Phe Ser Ala Gly
50 55 60

Asp Tyr Glu Ser Cys Ala Asp Ala Ala Val Val Ile Val Thr Gly Gly
65 70 75 80

Ala Asn Gln Lys Pro Gly Gln Thr Arg Met Glu Leu Ala Glu Arg Asn
85 90 95

Val Lys Ile Met Gln Glu Val Ile Pro Lys Ile Val Lys Tyr Ala Pro
100 105 110

Asn Ala Ile Leu Leu Ile Ala Thr Asn Pro Val Asp Val Leu Thr Tyr
115 120 125

Ala Ser Leu Lys Ala Ser Gly Phe Pro Ala Ser Arg Val Ile Gly Ser
130 135 140

Gly Thr Val Leu Asp Ser Ala Arg Ile Gln His Asn Leu Ser Lys Leu
145 150 155 160

Phe Asn Val Ser Ser Glu Ser Val Asn Ala Phe Ile Ile Gly Glu His
165 170 175

Gly Asp Ser Ser Val Pro Val Trp Ser Leu Ala Glu Ile Ala Gly Met
180 185 190

Lys Val Glu Asp Tyr Cys Arg Gln Ser Lys Arg Lys Phe Asp Pro Ser
195 200 205

Ile Leu Thr Lys Ile Tyr Glu Glu Ser Arg Asp Ala Ala Ala Tyr Ile

210

215

220

Ile Glu Arg Lys Gly Tyr Thr Asn Phe Gly Ile Ala Ala Gly Leu Ala
 225 230 235 240

Arg Ile Val Arg Ala Ile Leu Arg Asp Glu Gly Ala Leu Leu Thr Val
 245 250 255

Ser Thr Val Gly Glu His Phe Gly Met Lys Asp Val Ser Leu Ser Val
 260 265 270

Pro Thr Arg Val Asp Arg Ser Gly Ala His His Val Val Asp Leu Leu
 275 280 285

Leu Asn Asp Lys Glu Leu Glu Gln Ile Lys Thr Ser Gly Ala Lys Ile
 290 295 300

Lys Ser Ala Cys Asp Glu Leu Gly Ile
 305 310

<210> 31
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<400> 31
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<210> 41
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<213> Kluyveromyces thermotolerans

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240

ctattatcag ggccagaaaa aggaagtgtt tccctccttc ttgaattgat gttaccctca
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agaacaaaac tgaaaaaacc cagacacgct cgacttcctg tcttcctatt gattgcagct
420

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720

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1920

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1980

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2040

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2100

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<212> DNA
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<210> 46
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<212> DNA
<213> Candida albicans

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<210> 47
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<210> 49
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<210> 50
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<210> 51
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<210> 52
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<400> 52
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<210> 53
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<210> 55
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<210> 59
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<210> 60
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<212> DNA

<213> Candida sonorensis

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<210> 62

<211> 34

<212> DNA

<213> Candida sonorensis

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<213> Candida sonorensis

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<211> 36

<212> DNA

<213> Candida sonorensis

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<210> 65

<211> 35

<212> DNA

<213> Candida sonorensis

<400> 65

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35

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